



SEQUENCE LISTING

<110> Miao et al.

<120> METHOD OF TREATING DOPAMINERGIC AND GABA-NERGIC DISORDERS

<130> CIBT-P02-044

<140> 09/451939

<141> 1999-12-01

<150> 08/900220

<151> 1997-07-24

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<170> PatentIn Ver. 2.1

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 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
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 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
 355 360 365
 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
 370 375 380
 Ile Pro Thr Ala Ala Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
 385 390 395 400
 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His
 405 410 415
 Pro Leu Gly Met Val Ala Pro Ala Ser
 420 425
 <210> 11
 <211> 396
 <212> PRT
 <213> Mus musculus
 <400> 11
 Met Ala Leu Pro Ala Ser Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15
 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30
 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45
 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60
 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
85 90 95

Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
100 105 110

Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125

Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
130 135 140

Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
145 150 155 160

Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
165 170 175

Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
180 185 190

Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
195 200 205

Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
210 215 220

Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
225 230 235 240

Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
245 250 255

Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
260 265 270

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
290 295 300

Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Met Gly
385 390 395

<210> 12
<211> 411
<212> PRT
<213> Mus musculus

<400> 12
Met Ser Pro Ala Trp Leu Arg Pro Arg Leu Arg Phe Cys Leu Phe Leu
1 5 10 15

Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
115 120 125

Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
145 150 155 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
180 185 190

Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
195 200 205

Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
210 215 220

Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
225 230 235 240

Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
245 250 255

Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
260 265 270

Pro Ala His Leu Leu Phe Ile Ala Asp Asn His Thr Glu Pro Ala Ala

275

280

285

His Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300

Leu Val Ser Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320

Ser Thr His Val Ala Leu Gly Ser Tyr Ala Pro Leu Thr Arg His Gly
 325 330 335

Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350

Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe Pro
 355 360 365

Ser Leu Ala Trp Gly Ser Trp Thr Pro Ser Glu Gly Val His Ser Tyr
 370 375 380

Pro Gln Met Leu Tyr Arg Leu Gly Arg Leu Leu Glu Glu Ser Thr
 385 390 395 400

Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410

<210> 13

<211> 437

<212> PRT

<213> Mus musculus

<400> 13

Met Leu Leu Leu Leu Ala Arg Cys Phe Leu Val Ile Leu Ala Ser Ser
 1 5 10 15

Leu Leu Val Cys Pro Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly
 20 25 30

Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe
 35 40 45

Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu
 50 55 60

Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn
 65 70 75 80

Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp
 85 90 95

Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile
 100 105 110

Ser Val Met Asn Gln Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
 115 120 125

Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly
 130 135 140

Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly

145	150	155	160
Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr			
165	170	175	
Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val			
180	185	190	
Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu			
195	200	205	
Glu Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Arg Pro Gly Asp Arg			
210	215	220	
Val Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu			
225	230	235	240
Thr Phe Leu Asp Arg Asp Glu Gly Ala Lys Lys Val Phe Tyr Val Ile			
245	250	255	
Glu Thr Leu Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu			
260	265	270	
Leu Phe Val Ala Pro His Asn Asp Ser Gly Pro Thr Pro Gly Pro Ser			
275	280	285	
Ala Leu Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val			
290	295	300	
Ala Glu Arg Gly Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser			
305	310	315	320
Val Thr Leu Arg Glu Glu Ala Gly Ala Tyr Ala Pro Leu Thr Ala			
325	330	335	
His Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val			
340	345	350	
Ile Glu Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu			
355	360	365	
Ala His Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Gly Gly			
370	375	380	
Gly Gly Gly Ser Ile Pro Ala Ala Gln Ser Ala Thr Glu Ala Arg Gly			
385	390	395	400
Ala Glu Pro Thr Ala Gly Ile His Trp Tyr Ser Gln Leu Leu Tyr His			
405	410	415	
Ile Gly Thr Trp Leu Leu Asp Ser Glu Thr Met His Pro Leu Gly Met			
420	425	430	
Ala Val Lys Ser Ser			
435			

<210> 14

<211> 418

<212> PRT

<213> Brachydanio rerio

<400> 14

Met Arg Leu Leu Thr Arg Val Leu Leu Val Ser Leu Leu Thr Leu Ser
1 5 10 15

Leu Val Val Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Tyr Gly Arg
20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ser Leu Ala Ile Ser
100 105 110

Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Phe Glu Glu Ser Leu His Tyr Glu Gly Arg
130 135 140

Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys Tyr Gly Thr
145 150 155 160

Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu
165 170 175

Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala
180 185 190

Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Leu Val Ser Leu Gln
195 200 205

Asp Gly Gly Gln Lys Ala Val Lys Asp Leu Asn Pro Gly Asp Lys Val
210 215 220

Leu Ala Ala Asp Ser Ala Gly Asn Leu Val Phe Ser Asp Phe Ile Met
225 230 235 240

Phe Thr Asp Arg Asp Ser Thr Thr Arg Arg Val Phe Tyr Val Ile Glu
245 250 255

Thr Gln Glu Pro Val Glu Lys Ile Thr Leu Thr Ala Ala His Leu Leu
260 265 270

Phe Val Leu Asp Asn Ser Thr Glu Asp Leu His Thr Met Thr Ala Ala
275 280 285

Tyr Ala Ser Ser Val Arg Ala Gly Gln Lys Val Met Val Val Asp Asp
290 295 300

Ser Gly Gln Leu Lys Ser Val Ile Val Gln Arg Ile Tyr Thr Glu Glu
305 310 315 320

Gln Arg Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile Val Val
325 330 335

Asp Arg Ile Leu Ala Ser Cys Tyr Ala Val Ile Glu Asp Gln Gly Leu
340 345 350

Ala His Leu Ala Phe Ala Pro Ala Arg Leu Tyr Tyr Val Ser Ser
355 360 365

Phe Leu Ser Pro Lys Thr Pro Ala Val Gly Pro Met Arg Leu Tyr Asn
370 375 380

Arg Arg Gly Ser Thr Gly Thr Pro Gly Ser Cys His Gln Met Gly Thr
385 390 395 400

Trp Leu Leu Asp Ser Asn Met Leu His Pro Leu Gly Met Ser Val Asn
405 410 415

Ser Ser

<210> 15

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (463)

<223> Xaa=unknown amino acid residue

<400> 15

Met Leu Leu Leu Ala Arg Cys Leu Leu Leu Val Leu Val Ser Ser Leu
1 5 10 15

Leu Val Cys Ser Gly Leu Ala Cys Gly Pro Gly Arg Gly Phe Gly Lys
20 25 30

Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys Gln Phe Ile
35 40 45

Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg Tyr Glu Gly
50 55 60

Lys Ile Ser Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr Pro Asn Tyr
65 70 75 80

Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly Ala Asp Arg
85 90 95

Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu Ala Ile Ser
100 105 110

Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr Glu Gly Trp
115 120 125

Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr Glu Gly Arg

130	135	140
Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys Tyr Gly Met		
145	150	155
Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu		
165	170	175
Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn Ser Val Ala		
180	185	190
Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val His Leu Glu		
195	200	205
Gln Gly Gly Thr Lys Leu Val Lys Asp Leu Ser Pro Gly Asp Arg Val		
210	215	220
Leu Ala Ala Asp Asp Gln Gly Arg Leu Leu Tyr Ser Asp Phe Leu Thr		
225	230	235
Phe Leu Asp Arg Asp Gly Ala Lys Lys Val Phe Tyr Val Ile Glu		
245	250	255
Thr Arg Glu Pro Arg Glu Arg Leu Leu Leu Thr Ala Ala His Leu Leu		
260	265	270
Phe Val Ala Pro His Asn Asp Ser Ala Thr Gly Glu Pro Glu Ala Ser		
275	280	285
Ser Gly Ser Gly Pro Pro Ser Gly Gly Ala Leu Gly Pro Arg Ala Leu		
290	295	300
Phe Ala Ser Arg Val Arg Pro Gly Gln Arg Val Tyr Val Val Ala Glu		
305	310	315
Arg Asp Gly Asp Arg Arg Leu Leu Pro Ala Ala Val His Ser Val Thr		
325	330	335
Leu Ser Glu Glu Ala Ala Gly Ala Tyr Ala Pro Leu Thr Ala Gln Gly		
340	345	350
Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys Tyr Ala Val Ile Glu		
355	360	365
Glu His Ser Trp Ala His Arg Ala Phe Ala Pro Phe Arg Leu Ala His		
370	375	380
Ala Leu Leu Ala Ala Leu Ala Pro Ala Arg Thr Asp Arg Gly Gly Asp		
385	390	395
Ser Gly Gly Asp Arg Gly Gly Gly Arg Val Ala Leu Thr		
405	410	415
Ala Pro Gly Ala Ala Asp Ala Pro Gly Ala Gly Ala Thr Ala Gly Ile		
420	425	430
His Trp Tyr Ser Gln Leu Leu Tyr Gln Ile Gly Thr Trp Leu Leu Asp		
435	440	445
Ser Glu Ala Leu His Pro Leu Gly Met Ala Val Lys Ser Ser Xaa Ser		

450

455

460

Arg Gly Ala Gly Gly Ala Arg Glu Gly Ala
 465 470 475

<210> 16
 <211> 411
 <212> PRT
 <213> Homo sapiens

<400> 16
 Met Ser Pro Ala Arg Leu Arg Pro Arg Leu His Phe Cys Leu Val Leu
 1 5 10 15

Leu Leu Leu Leu Val Val Pro Ala Ala Trp Gly Cys Gly Pro Gly Arg
 20 25 30

Val Val Gly Ser Arg Arg Arg Pro Pro Arg Lys Leu Val Pro Leu Ala
 35 40 45

Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
 50 55 60

Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
 65 70 75 80

Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
 85 90 95

Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
 100 105 110

Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
 115 120 125

Val Thr Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
 130 135 140

His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
 145 150 155 160

Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
 165 170 175

Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
 180 185 190

Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
 195 200 205

Gln Val Arg Leu Glu Ser Gly Ala Arg Val Ala Leu Ser Ala Val Arg
 210 215 220

Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Ser Pro Thr Phe
 225 230 235 240

Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro His Arg Leu Arg Ala
 245 250 255

Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
 260 265 270
 Pro Ala His Leu Leu Phe Thr Ala Asp Asn His Thr Glu Pro Ala Ala
 275 280 285
 Arg Phe Arg Ala Thr Phe Ala Ser His Val Gln Pro Gly Gln Tyr Val
 290 295 300
 Leu Val Ala Gly Val Pro Gly Leu Gln Pro Ala Arg Val Ala Ala Val
 305 310 315 320
 Ser Thr His Val Ala Leu Gly Ala Tyr Ala Pro Leu Thr Lys His Gly
 325 330 335
 Thr Leu Val Val Glu Asp Val Val Ala Ser Cys Phe Ala Ala Val Ala
 340 345 350
 Asp His His Leu Ala Gln Leu Ala Phe Trp Pro Leu Arg Leu Phe His
 355 360 365
 Ser Leu Ala Trp Gly Ser Trp Thr Pro Gly Glu Gly Val His Trp Tyr
 370 375 380
 Pro Gln Leu Leu Tyr Arg Leu Gly Arg Leu Leu Leu Glu Glu Gly Ser
 385 390 395 400
 Phe His Pro Leu Gly Met Ser Gly Ala Gly Ser
 405 410
 <210> 17
 <211> 396
 <212> PRT
 <213> Homo sapiens
 <400> 17
 Met Ala Leu Leu Thr Asn Leu Leu Pro Leu Cys Cys Leu Ala Leu Leu
 1 5 10 15
 Ala Leu Pro Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
 20 25 30
 Arg Arg Tyr Ala Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
 35 40 45
 Val Pro Gly Val Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
 50 55 60
 Gly Arg Val Ala Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
 65 70 75 80
 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
 85 90 95

Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
100 105 110

Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
115 120 125

Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
130 135 140

Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
145 150 155 160

Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
165 170 175

Glu Ser Arg Asn His Val His Val Ser Val Lys Ala Asp Asn Ser Leu
180 185 190

Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
195 200 205

Trp Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
210 215 220

Val Leu Ala Ala Asp Ala Ser Gly Arg Val Val Pro Thr Pro Val Leu
225 230 235 240

Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
245 250 255

Glu Thr Glu Trp Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
260 265 270

Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
275 280 285

Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
290 295 300

Gly Asp Ala Leu Arg Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
305 310 315 320

Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
325 330 335

Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
340 345 350

Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
355 360 365

Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
370 375 380

Arg Leu Leu Tyr Arg Leu Ala Glu Glu Leu Leu Gly
385 390 395

<210> 18
<211> 416
<212> PRT
<213> Brachydanio rerio

<400> 18
Met Asp Val Arg Leu His Leu Lys Gln Phe Ala Leu Leu Cys Phe Ile
1 5 10 15

Ser Leu Leu Leu Thr Pro Cys Gly Leu Ala Cys Gly Pro Gly Arg Gly
20 25 30

Tyr Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys
35 40 45

Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Lys
50 55 60

Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Ile
65 70 75 80

Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Asn
85 90 95

Ala Asp Arg Leu Met Thr Lys Arg Cys Lys Asp Lys Leu Asn Ser Leu
100 105 110

Ala Ile Ser Val Met Asn His Trp Pro Gly Val Lys Leu Arg Val Thr
115 120 125

Glu Gly Trp Asp Glu Asp Gly His His Leu Glu Glu Ser Leu His Tyr
130 135 140

Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Lys Ser Lys
145 150 155 160

Tyr Gly Met Leu Ser Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
165 170 175

Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
180 185 190

Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Gly Thr Val

195	200	205
Thr Leu Gly Asp Gly Thr Arg Lys Pro Ile Lys Asp Leu Lys Val Gly		
210	215	220
Asp Arg Val Leu Ala Ala Asp Glu Lys Gly Asn Val Leu Ile Ser Asp		
225	230	235
Phe Ile Met Phe Ile Asp His Asp Pro Thr Thr Arg Arg Gln Phe Ile		
245	250	255
Val Ile Glu Thr Ser Glu Pro Phe Thr Lys Leu Thr Leu Thr Ala Ala		
260	265	270
His Leu Val Phe Val Gly Asn Ser Ser Ala Ala Ser Gly Ile Thr Ala		
275	280	285
Thr Phe Ala Ser Asn Val Lys Pro Gly Asp Thr Val Leu Val Trp Glu		
290	295	300
Asp Thr Cys Glu Ser Leu Lys Ser Val Thr Val Lys Arg Ile Tyr Thr		
305	310	315
Glu Glu His Glu Gly Ser Phe Ala Pro Val Thr Ala His Gly Thr Ile		
325	330	335
Ile Val Asp Gln Val Leu Ala Ser Cys Tyr Ala Val Ile Glu Asn His		
340	345	350
Lys Trp Ala His Trp Ala Phe Ala Pro Val Arg Leu Cys His Lys Leu		
355	360	365
Met Thr Trp Leu Phe Pro Ala Arg Glu Ser Asn Val Asn Phe Gln Glu		
370	375	380
Asp Gly Ile His Trp Tyr Ser Asn Met Leu Phe His Ile Gly Ser Trp		
385	390	395
Leu Leu Asp Arg Asp Ser Phe His Pro Leu Gly Ile Leu His Leu Ser		
405	410	415

<210> 19
 <211> 1416
 <212> DNA
 <213> Drosophila melanogaster

<220>
 <221> CDS
 <222> (1)...(1413)

<400> 19
 atg gat aac cac agc tca gtg cct tgg gcc agt gcc gcc agt gtc acc 48
 Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr
 1 5 10 15
 tgt ctc tcc ctg gga tgc caa atg cca cag ttc cag ttc cag 96
 Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln
 20 25 30

ctc caa atc cgc agc gag ctc cat ctc cgc aag ccc gca aga aga acg Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr	35	40	45	144
caa acg atg cgc cac att gcg cat acg cag cgt tgc ctc agc agg ctg Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu	50	55	60	192
acc tct ctg gtg gcc ctg ctg atc gtc ttg ccg atg gtc ttt agc Thr Ser Leu Val Ala Leu Leu Ile Val Leu Pro Met Val Phe Ser	65	70	75	240
ccg gct cac agc tgc ggt cct ggc cga gga ttg ggt cgt cat agg gcg Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala	85	90	95	288
ccg aac ctg tat ccg ctg gtc ctc aag cag aca att ccc aat cta tcc Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser	100	105	110	336
gag tac acg aac agc gcc tcc gga cct ctg gag ggt gtg atc cgt cgg Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg	115	120	125	384
gat tcg ccc aaa ttc aag gac ctc gtg ccc aac tac aac agg gac atc Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile	130	135	140	432
ctt ttc cgt gac gag gaa ggc acc gga gcg gat ggc ttg atg agc aag Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys	145	150	155	480
160				
ccg tgc aag gag aag cta aac gtg ctg gcc tac tcg gtg atg aac gaa Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu	165	170	175	528
tgg ccc ggc atc cgg ctg gtc acc gag agc tgg gac gag gac tac Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr	180	185	190	576
cat cac ggc cag gag tcg ctc cac tac gag ggc cga gcg gtg acc att His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile	195	200	205	624
gcc acc tcc gat cgc gac cag tcc aaa tac ggc atg ctc gct cgc ctg Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu	210	215	220	672
225				
gcc gtc gag gct gga ttc gat tgg gtc tcc tac gtc agc agg cgc cac Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His	230	235	240	720
245				
atc tac tgc tcc gtc aag tca gat tcg tcg atc agt tcc cac gtg cac Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His	250	255	260	768
260	265	270		816

aag ccg ctc ggc gag ctc tct atc gga gat cgt gtt ttg agc atg acc		864	
Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr			
275	280	285	
gcc aac gga cag gcc gtc tac agc gaa gtg atc ctc ttc atg gac cgc		912	
Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg			
290	295	300	
aac ctc gag cag atg caa aac ttt gtg cag ctg cac acg gac ggt gga		960	
Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly			
305	310	315	320
gca gtg ctc acg gtg acg ccg gct cac ctg gtt agc gtt tgg cag ccg		1008	
Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro			
325	330	335	
gag agc cag aag ctc acg ttt gtg ttt gcg cat cgc atc gag gag aag		1056	
Glu Ser Gln Lys Leu Thr Phe Val Ala His Arg Ile Glu Glu Lys			
340	345	350	
aac cag gtg ctc gta cgg gat gtg gag acg ggc gag ctg agg ccc cag		1104	
Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln			
355	360	365	
cga gtg gtc aag ttg ggc agt gtg cgc agt aag ggc gtg gtc gcg ccg		1152	
Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro			
370	375	380	
ctg acc cgc gag ggc acc att gtg gtc aac tcg gtg gcc gac agt tgc		1200	
Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys			
385	390	395	400
tat gcg gtg atc aac agt cag tcg ctg gcc cac tgg gga ctg gct ccc		1248	
Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro			
405	410	415	
atg cgc ctg ctg tcc acg ctg gag gcg tgg ctg ccc gcc aag gag cag		1296	
Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln			
420	425	430	
ttg cac agt tcg ccg aag gtg gtg agc tcg gcg cag cag cag aat ggc		1344	
Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly			
435	440	445	
atc cat tgg tat gcc aat gcg ctc tac aag gtc aag gac tac gtg ctg		1392	
Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu			
450	455	460	
ccg cag agc tgg cgc cac gat tga		1416	
Pro Gln Ser Trp Arg His Asp			
465	470		

<210> 20

<211> 471

<212> PRT

<213> Drosophila melanogaster

<400> 20

Met Asp Asn His Ser Ser Val Pro Trp Ala Ser Ala Ala Ser Val Thr

1	5	10	15
Cys Leu Ser Leu Gly Cys Gln Met Pro Gln Phe Gln Phe Gln			
20	25	30	
Leu Gln Ile Arg Ser Glu Leu His Leu Arg Lys Pro Ala Arg Arg Thr			
35	40	45	
Gln Thr Met Arg His Ile Ala His Thr Gln Arg Cys Leu Ser Arg Leu			
50	55	60	
Thr Ser Leu Val Ala Leu Leu Ile Val Leu Pro Met Val Phe Ser			
65	70	75	80
Pro Ala His Ser Cys Gly Pro Gly Arg Gly Leu Gly Arg His Arg Ala			
85	90	95	
Arg Asn Leu Tyr Pro Leu Val Leu Lys Gln Thr Ile Pro Asn Leu Ser			
100	105	110	
Glu Tyr Thr Asn Ser Ala Ser Gly Pro Leu Glu Gly Val Ile Arg Arg			
115	120	125	
Asp Ser Pro Lys Phe Lys Asp Leu Val Pro Asn Tyr Asn Arg Asp Ile			
130	135	140	
Leu Phe Arg Asp Glu Glu Gly Thr Gly Ala Asp Gly Leu Met Ser Lys			
145	150	155	160
Arg Cys Lys Glu Lys Leu Asn Val Leu Ala Tyr Ser Val Met Asn Glu			
165	170	175	
Trp Pro Gly Ile Arg Leu Leu Val Thr Glu Ser Trp Asp Glu Asp Tyr			
180	185	190	
His His Gly Gln Glu Ser Leu His Tyr Glu Gly Arg Ala Val Thr Ile			
195	200	205	
Ala Thr Ser Asp Arg Asp Gln Ser Lys Tyr Gly Met Leu Ala Arg Leu			
210	215	220	
Ala Val Glu Ala Gly Phe Asp Trp Val Ser Tyr Val Ser Arg Arg His			
225	230	235	240
Ile Tyr Cys Ser Val Lys Ser Asp Ser Ser Ile Ser Ser His Val His			
245	250	255	
Gly Cys Phe Thr Pro Glu Ser Thr Ala Leu Leu Glu Ser Gly Val Arg			
260	265	270	
Lys Pro Leu Gly Glu Leu Ser Ile Gly Asp Arg Val Leu Ser Met Thr			
275	280	285	
Ala Asn Gly Gln Ala Val Tyr Ser Glu Val Ile Leu Phe Met Asp Arg			
290	295	300	
Asn Leu Glu Gln Met Gln Asn Phe Val Gln Leu His Thr Asp Gly Gly			
305	310	315	320

Ala Val Leu Thr Val Thr Pro Ala His Leu Val Ser Val Trp Gln Pro
 325 330 335

 Glu Ser Gln Lys Leu Thr Phe Val Phe Ala His Arg Ile Glu Glu Lys
 340 345 350

 Asn Gln Val Leu Val Arg Asp Val Glu Thr Gly Glu Leu Arg Pro Gln
 355 360 365

 Arg Val Val Lys Leu Gly Ser Val Arg Ser Lys Gly Val Val Ala Pro
 370 375 380

 Leu Thr Arg Glu Gly Thr Ile Val Val Asn Ser Val Ala Ala Ser Cys
 385 390 395 400

 Tyr Ala Val Ile Asn Ser Gln Ser Leu Ala His Trp Gly Leu Ala Pro
 405 410 415

 Met Arg Leu Leu Ser Thr Leu Glu Ala Trp Leu Pro Ala Lys Glu Gln
 420 425 430

 Leu His Ser Ser Pro Lys Val Val Ser Ser Ala Gln Gln Gln Asn Gly
 435 440 445

 Ile His Trp Tyr Ala Asn Ala Leu Tyr Lys Val Lys Asp Tyr Val Leu
 450 455 460

 Pro Gln Ser Trp Arg His Asp
 465 470

<210> 21
 <211> 221
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Degenerate Shh
 polypeptide general formula

 <220>
 <221> SITE
 <222> (7)
 <223> Xaa=Gly, Ala, Val, Leu, Ile, Phe, Tyr, or Trp

 <220>
 <221> SITE
 <222> (9)
 <223> Xaa=Arg, His or Lys

 <220>
 <221> SITE
 <222> (44)
 <223> Xaa=Gly, Ala, Val, Leu, Ile, Ser. or Thr

 <220>
 <221> SITE
 <222> (85)
 <223> Xaa=Gly, Ala, Val, Leu, Ile, Ser, or Thr

<220>
<221> SITE
<222> (93)
<223> Xaa=Lys, Arg, His, Asn, or Gln

<220>
<221> SITE
<222> (98)
<223> Xaa=Lys, Arg or His

<220>
<221> SITE
<222> (112)
<223> Xaa=Ser, Thr, Tyr, Trp, or Phe

<220>
<221> SITE
<222> (132)
<223> Xaa=Lys, Arg or His

<220>
<221> SITE
<222> (137)
<223> Xaa=Met, Cys, Ser, or Thr

<220>
<221> SITE
<222> (139)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Ser, or Thr

<220>
<221> SITE
<222> (181)
<223> Xaa=Leu, Val, Met, Thr, or Ser

<220>
<221> SITE
<222> (183)
<223> Xaa=His, Phe, Tyr, Ser, Thr, Met, or Cys

<220>
<221> SITE
<222> (185)
<223> Xaa=Gln, Asn, Glu, or Asp

<220>
<221> SITE
<222> (186)
<223> Xaa=His, Phe, Tyr, Thr, Gln, Asn, Glu, or Asp

<220>
<221> SITE
<222> (189)
<223> Xaa=Gln, Asn, Glu, Asp, Thr, Ser, Met, or Cys

<220>
<221> SITE
<222> (191)
<223> Xaa=Ala, Gly, Cys, Leu, Val, or Met

<220>
<221> SITE
<222> (196)
<223> Xaa=Arg, Lys, Met, Ile, Asn, Asp, Glu, Gln, Ser,
Thr, or Cys

<220>
<221> SITE
<222> (200)
<223> Xaa=Arg, Lys, Met, or Ile

<220>
<221> SITE
<222> (206)
<223> Xaa=Ala, Gly, Cys, Asp, Glu, Gln, Asn, Ser, Thr,
or Met

<220>
<221> SITE
<222> (207)
<223> Xaa=Ala, Gly, Cys, Asp, Asn, Glu, or Gln

<220>
<221> SITE
<222> (209)
<223> Xaa=Arg, Lys, Met, Ile, Asn, Asp, or Glu

<220>
<221> SITE
<222> (211)
<223> Xaa=Leu, Val, Met, or Ile

<220>
<221> SITE
<222> (212)
<223> Xaa=Phe, Tyr, Thr, His, or Trp

<220>
<221> SITE
<222> (216)
<223> Xaa=Ile, Val, Leu, or Met

<220>
<221> SITE
<222> (217)
<223> Xaa=Met, Cys, Ile, Leu, Val, Thr, or Ser

<220>
<221> SITE
<222> (219)
<223> Xaa=Leu, Val, Met, Thr, or Ser

<400> 21
Cys Gly Pro Gly Arg Gly Xaa Gly Xaa Arg Arg His Pro Lys Lys Leu
1 5 10 15

Thr Pro Leu Ala Tyr Lys Gln Phe Ile Pro Asn Val Ala Glu Lys Thr
20 25 30

Leu Gly Ala Ser Gly Arg Tyr Glu Gly Lys Ile Xaa Arg Asn Ser Glu

35

40

45

Arg Phe Lys Glu Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys
 50 55 60

Asp Glu Glu Asn Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys
 65 70 75 80

Asp Lys Leu Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp Pro Gly
 85 90 95

Val Xaa Leu Arg Val Thr Glu Gly Trp Asp Glu Asp Gly His His Xaa
 100 105 110

Glu Glu Ser Leu His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser
 115 120 125

Asp Arg Asp Xaa Ser Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala Val Glu
 130 135 140

Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Lys Ala His Ile His Cys
 145 150 155 160

Ser Val Lys Ala Glu Asn Ser Val Ala Ala Lys Ser Gly Gly Cys Phe
 165 170 175

Pro Gly Ser Ala Xaa Val Xaa Leu Xaa Xaa Gly Gly Xaa Lys Xaa Val
 180 185 190

Lys Asp Leu Xaa Pro Gly Asp Xaa Val Leu Ala Ala Asp Xaa Xaa Gly
 195 200 205

Xaa Leu Xaa Xaa Ser Asp Phe Xaa Xaa Phe Xaa Asp Arg
 210 215 220

<210> 22

<211> 167

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Degenerate hedgehog polypeptide general formula

<220>

<221> SITE

<222> (7)

<223> Xaa=Gly, Ala, Val, Leu, Ile, Pro, Phe, or Tyr

<220>

<221> SITE

<222> (8)

<223> Xaa=Gly, Ala, Val, Leu, or Ile

<220>

<221> SITE

<222> (9)

<223> Xaa=Gly, Ala, Val, Leu, Ile, Lys, His, or Arg

<220>
<221> SITE
<222> (12)
<223> Xaa=Lys, Arg or His

<220>
<221> SITE
<222> (13)
<223> Xaa=Phe, Trp or Tyr or an amino acid gap

<220>
<221> SITE
<222> (14)
<223> Xaa=Gly, Ala, Val, Leu, or Ile or an amino acid gap

<220>
<221> SITE
<222> (17)
<223> Xaa=Asn, Gln, His, Arg, or Lys

<220>
<221> SITE
<222> (19)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Ser, or Thr

<220>
<221> SITE
<222> (22)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Ser, or Thr

<220>
<221> SITE
<222> (27)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Ser, or Thr

<220>
<221> SITE
<222> (29)
<223> Xaa=Ser, Thr, Gln, or Asn

<220>
<221> SITE
<222> (30)
<223> Xaa=Met, Cys, Gly, Ala, Val, Leu, Ile, Ser, or Thr

<220>
<221> SITE
<222> (31)
<223> Xaa=Gly, Alka, Val, Leu, Ile, or Pro

<220>
<221> SITE
<222> (33)
<223> Xaa=Arg, His or Lys

<220>
<221> SITE
<222> (40)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Pro Arg, His, or Lys

<220>
<221> SITE
<222> (41)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Phe, or Tyr

<220>
<221> SITE
<222> (44)
<223> Xaa=Arg, His or Lys

<220>
<221> SITE
<222> (45)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Ser, or Thr

<220>
<221> SITE
<222> (46)
<223> Xaa=Thr or Ser

<220>
<221> SITE
<222> (48)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Asn, or Gln

<220>
<221> SITE
<222> (53)
<223> Xaa=Arg, His or Lys

<220>
<221> SITE
<222> (54)
<223> Xaa=Asp or Glu

<220>
<221> SITE
<222> (71)
<223> Xaa=Ser or Thr

<220>
<221> SITE
<222> (79)
<223> Xaa=Glu, Asp, Gln, or Asn

<220>
<221> SITE
<222> (83)
<223> Xaa=Glu or Asp

<220>
<221> SITE
<222> (84)
<223> Xaa=Arg, His or Lys

<220>
<221> SITE
<222> (85)
<223> Xaa=Gly, Ala, Val, Leu, or Ile

<220>
<221> SITE
<222> (87)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Thr, or Ser

<220>
<221> SITE
<222> (95)
<223> Xaa=Met, Cys, Gln, Asn, Arg, Lys, or His

<220>
<221> SITE
<222> (100)
<223> Xaa=Arg, His or Lys

<220>
<221> SITE
<222> (107)
<223> Xaa=Trp, Phe, Tyr, Arg, His, or Lys

<220>
<221> SITE
<222> (114)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Ser, Thr, Tyr, or Phe

<220>
<221> SITE
<222> (115)
<223> Xaa=Gln, Asn, Asp, or Glu

<220>
<221> SITE
<222> (116)
<223> Xaa=Asp or Glu

<220>
<221> SITE
<222> (125)
<223> Xaa=Gly, Ala, Val, Leu, or Ile

<220>
<221> SITE
<222> (134)
<223> Xaa=Arg, His or Lys

<220>
<221> SITE
<222> (135)
<223> Xaa=Asn, Gln, Thr, or Ser

<220>
<221> SITE
<222> (139)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, or Cys

<220>
<221> SITE
<222> (141)
<223> Xaa=Gly, Ala, Val, Leu, Ile, Thr, or Ser

<220>
 <221> SITE
 <222> (157)
 <223> Xaa=Arg, His or Lys

<220>
 <221> SITE
 <222> (158)
 <223> Xaa=Asn, Gln, Gly, Ala, Val, Leu, or Ile

<220>
 <221> SITE
 <222> (160)
 <223> Xaa=Gly, Ala, Val, Leu, or Ile

<220>
 <221> SITE
 <222> (162)..(162)
 <223> Xaa=Gly, Ala, Val, Leu, Ile, Ser, Thr, or Cys

<220>
 <221> SITE
 <222> (166)
 <223> Xaa=Gly, Ala, Val, Leu, Ile, Thr, or Ser

<220>
 <221> SITE
 <222> (167)
 <223> Xaa=Asp or Glu

<400> 22.
 Cys Gly Pro Gly Arg Gly Xaa Xaa Xaa Arg Arg Xaa Xaa Xaa Pro Lys
 1 5 10 15

Xaa Leu Xaa Pro Leu Xaa Tyr Lys Gln Phe Xaa Pro Xaa Xaa Xaa Glu
 20 25 30

Xaa Thr Leu Gly Ala Ser Gly Xaa Xaa Glu Gly Xaa Xaa Xaa Arg Xaa
 35 40 45

Ser Glu Arg Phe Xaa Xaa Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile
 50 55 60

Phe Lys Asp Glu Glu Asn Xaa Gly Ala Asp Arg Leu Met Thr Xaa Arg
 65 70 75 80

Cys Lys Xaa Xaa Xaa Asn Xaa Leu Ala Ile Ser Val Met Asn Xaa Trp
 85 90 95

Pro Gly Val Xaa Leu Arg Val Thr Glu Gly Xaa Asp Glu Asp Gly His
 100 105 110

His Xaa Xaa Xaa Ser Leu His Tyr Glu Gly Arg Ala Xaa Asp Ile Thr
 115 120 125

Thr Ser Asp Arg Asp Xaa Xaa Lys Tyr Gly Xaa Leu Xaa Arg Leu Ala
 130 135 140

Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr Glu Ser Xaa Xaa His Xaa

145	150	155	160
His Xaa Ser Val Lys Xaa Xaa			
165			
<210> 23			
<211> 74			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> primer			
<400> 23			
gcgcgcctcg aagcgaggca gccagcgagg gagagagcga gcgggcgagc cggagcgagg			60
aaatcgatgc gcgc			74
<210> 24			
<211> 74			
<212> DNA			
<213> Artificial Sequence			
<220>			
<223> primer			
<400> 24			
gcgcgcagat ctggaaagc gcaagagaga ggcacacgc acacacccgc cgccgcact			60
cgggatccgc gcgc			74
<210> 25			
<211> 996			
<212> DNA			
<213> Homo sapiens			
<400> 25			
cgaaggcagg cagccagcga gggagagagc gagcggcga gccggagcga ggaaatcga			60
ggttcgaatc cttcccccac caccatcaact ttcaaaaatgc cgaaagaatc tgctccctgc			120
tttgtgttg gaggtcgctg agtagtgcgc gagtaaaatt taagctaca caaggcaagg			180
cttgaccgac aattgcatga agaatctgct tagggtagg cgaaaaatgc tgcttcgcga			240
tgtacgggcc agatatacgc gttgacattt attattgact agttattaat agtaatcaat			300
tacggggtca ttatgtcata gccccatataat ggagttccgc gttacataac ttacggtaaa			360
tggcccgct ggctgaccgc ccaacgaccc ccgcattt acgtcaataa tgacgtatgt			420
tcccatagta acgccaatag ggactttcca ttgtacgtcaa tgggtggact attacggta			480
aactgcccac ttggcagtac atcaagtgtt tcatatgcca agtacgcccc ctattgacgt			540
caatgacggt aaatggcccg cctggcattt tgcccaatgtac atgaccttat gggactttcc			600
tacttggcag tacatctacg tattagtcat cgctattacc atggtgatgc ggtttggca			660

gtacatcaat gggcgtggat agcggttga ctcacgggga tttccaagtc tccacccat 720
tgacgtcaat gggagttgt tttggcacca aaatcaacgg gactttccaa aatgtcgtaa 780
caactccgcc ccattgacgc aaatgggcgg taggcgtgta cggtgggagg tctatataag 840
cagagctctc tggctaacta gagaacccac tgcttactgg cttatcgaaa ttaatacgac 900
tcactatagg gagacccaag ctgggtaccg agctcgatc gatctggaa agcgcaagag 960
agagcgcaca cgcacacacc cgccgcgcgc actcg 996

<210> 26
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-sense construct

<400> 26
gtccctggcgc cgccgcccgtc 26

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-sense construct

<400> 27
ttccgatgac cggccttcg cggta 26

<210> 28
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> anti-sense construct

<400> 28
gtgcacggaa aggtgcaggc cacact 26

<210> 29
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 29
ggctccggta tgtgc 15

<210> 30
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
ggctccggta tgtgc 15

<210> 31
<211> 25
<212> DNA
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<220>
<223> primer

<400> 31
cattggcagg aggagttgat tgtgg 25

<210> 32
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 32
agcacctttt gagtgaggatt tgggg 25

35